

0590

0129

#2



OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/036,568

DATE: 01/30/2002

TIME: 18:27:37

Input Set : N:\Crf3\RULE60\10036568.raw

Output Set: N:\CRF3\01302002\J036568.raw

1 <110> APPLICANT: Willson, Tracy  
 2 Nicola, Nicos A.  
 3 Hilton, Douglas J.  
 4 Metcalf, Donald  
 5 Zhang, Jian G.  
 6 <120> TITLE OF INVENTION: NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES  
 7 ENCODING SAME  
 8 <130> FILE REFERENCE: Davies cc  
 9 <140> CURRENT APPLICATION NUMBER: 10/036,568  
 10 <141> CURRENT FILING DATE: 2001-11-07  
 12 <150> PRIOR APPLICATION NUMBER: US/09/051,843  
 13 <151> PRIOR FILING DATE: 1998-06-29  
 16 <160> NUMBER OF SEQ ID NOS: 11  
 17 <170> SOFTWARE: PatentIn Ver. 2.0  
 19 <210> SEQ ID NO: 1  
 20 <211> LENGTH: 1383  
 21 <212> TYPE: DNA  
 22 <213> ORGANISM: nuc. & predicted a.a. seq. of mNR4  
 23 <220> FEATURE:  
 24 <221> NAME/KEY: CDS  
 25 <222> LOCATION: (61)..(1338)  
 26 <221> NAME/KEY: unsure  
 27 <222> LOCATION: (121)  
 28 <223> OTHER INFORMATION: n=authors are unsure of exact sequence in this  
 29 region  
 30 <221> NAME/KEY: unsure  
 31 <222> LOCATION: (122)  
 32 <223> OTHER INFORMATION: n=authors are unsure of exact sequence in this  
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 34 <221> NAME/KEY: unsure  
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 36 <223> OTHER INFORMATION: n=authors are unsure of exact sequence in this  
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 45 region  
 46 <221> NAME/KEY: unsure  
 47 <222> LOCATION: (642)

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52 atg gcg cgg cca gcg ctg ctg ggc gag ctg ttg gtg ctg cta ctg tgg 108
53 Met Ala Arg Pro Ala Leu Leu Gly Glu Leu Leu Val Leu Leu Leu Trp
54 1 5 10 15
W--> 55 acc gcc acc gtg nnn ggc caa gtt gcc gcg gcc aca gaa gtt cag cca 156
W--> 56 Thr Ala Thr Val Xaa Gly Gln Val Ala Ala Ala Thr Glu Val Gln Pro
57 20 25 30
58 cct gtg acg aat ttg agc gtc tct gtc gaa aat ctc tgc acg ata ata 204
59 Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Ile Ile
60 35 40 45
61 tgg acg tgg agt cct cct gaa gga gcc agt cca aat tgc act ctc aga 252
62 Trp Thr Trp Ser Pro Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg
63 50 55 60
64 tat ttt agt cac ttt gat gac caa cag gat aag aaa att gct cca gaa 300
65 Tyr Phe Ser His Phe Asp Asp Gln Gln Asp Lys Lys Ile Ala Pro Glu
66 65 70 75 80
67 act cat cgt aaa gag gaa tta ccc ctg gat gag aaa atc tgt ctg cag 348
68 Thr His Arg Lys Glu Glu Leu Pro Leu Asp Glu Lys Ile Cys Leu Gln
69 85 90 95
70 gtg ggc tct cag tgt agt gcc aat gaa agt gag aag cct agc cct ttg 396
71 Val Gly Ser Gln Cys Ser Ala Asn Glu Ser Glu Lys Pro Ser Pro Leu
72 100 105 110
73 gtg aaa aag tgc atc tca ccc cct gaa ggt gat cct gag tcc gct gtg 444
74 Val Lys Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val
75 115 120 125
76 act gag ctc aag tgc att tgg cat aac ctg agc tat atg aag tgt tcc 492
77 Thr Glu Leu Lys Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser
78 130 135 140
79 tgg ctc cct gga agg aat aca agc cct gac aca cac tat act ctg tac 540
80 Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr His Tyr Thr Leu Tyr
81 145 150 155 160
82 tat tgg tac agc agc ctg gag aaa agt cgt caa tgt gaa aac atc tat 588
83 Tyr Trp Tyr Ser Ser Leu Glu Lys Ser Arg Gln Cys Glu Asn Ile Tyr
84 165 170 175
85 aga gaa ggt caa cac att gct tgt tcc ttt aaa ttg act aaa gtg gaa 636
86 Arg Glu Gly Gln His Ile Ala Cys Ser Phe Lys Leu Thr Lys Val Glu
87 180 185 190
W--> 88 cct nnn agt ttt gaa cat cag aac gtt caa ata atg gtc aag gat aat 684
W--> 89 Pro Xaa Ser Phe Glu His Gln Asn Val Gln Ile Met Val Lys Asp Asn
90 195 200 205
91 gct ggg aaa att agg cca tcc tgc aaa ata gtg tct tta act tcc tat 732
92 Ala Gly Lys Ile Arg Pro Ser Cys Lys Ile Val Ser Leu Thr Ser Tyr
93 210 215 220
94 gtg aaa cct gat cct cca cat att aaa cat ctt ctc ctc aaa aat ggt 780
95 Val Lys Pro Asp Pro Pro His Ile Lys His Leu Leu Leu Lys Asn Gly
96 225 230 235 240

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97      gcc tta tta gtg.cag tgg aag aat cca caa aat ttt aga agc aga tgc      828
98      Ala Leu Leu Val Gln Trp Lys Asn Pro Gln Asn Phe Arg Ser Arg Cys
99              245              250              255
100     tta act tat gaa gtg gag gtc aat aat act caa acc gac cga cat aat      876
101     Leu Thr Tyr Glu Val Glu Val Asn Asn Thr Gln Thr Asp Arg His Asn
102              260              265              270
103     att tta gag gtt gaa gag gac aaa tgc cag aat tcc gaa tct gat aga      924
104     Ile Leu Glu Val Glu Glu Asp Lys Cys Gln Asn Ser Glu Ser Asp Arg
105              275              280              285
106     aac atg gag ggt aca agt tgt ttc caa ctc cct ggt gtt ctt gcc gac      972
107     Asn Met Glu Gly Thr Ser Cys Phe Gln Leu Pro Gly Val Leu Ala Asp
108              290              295              300
109     gct gtc tac aca gtc aga gta aga gtc aaa aca aac aag tta tgc ttt      1020
110     Ala Val Tyr Thr Val Arg Val Arg Val Lys Thr Asn Lys Leu Cys Phe
111     305              310              315              320
112     gat gac aac aaa ctg tgg agt gat tgg agt gaa gca cag agt ata ggt      1068
113     Asp Asp Asn Lys Leu Trp Ser Asp Trp Ser Glu Ala Gln Ser Ile Gly
114              325              330              335
115     aag gag caa aac tcc acc ttc tac acc acc atg tta ctc acc att cca      1116
116     Lys Glu Gln Asn Ser Thr Phe Tyr Thr Thr Met Leu Leu Thr Ile Pro
117              340              345              350
118     gtc ttt gtc gca gtg gca gtc ata atc ctc ctt ttt tac ctg aaa agg      1164
119     Val Phe Val Ala Val Ala Val Ile Ile Leu Leu Phe Tyr Leu Lys Arg
120              355              360              365
121     ctt aag atc att ata ttt cct cca att cct gat cct ggc aag att ttt      1212
122     Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe
123     370              375              380
124     aaa gaa atg ttt gga gac cag aat gat gat acc ctg cac tgg aag aag      1260
125     Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys
126     385              390              395              400
127     tat gac atc tat gag aaa caa tcc aaa gaa gaa acg gat tct gta gtg      1308
128     Tyr Asp Ile Tyr Glu Lys Gln Ser Lys Glu Glu Thr Asp Ser Val Val
129              405              410              415
130     ctg ata gaa aac ctg aag aaa gca gct cct tgatggggag aagtgatttc      1358
131     Leu Ile Glu Asn Leu Lys Lys Ala Ala Pro
132              420              425
133     tttcttgccct tcaatgtgac cctgt      1383
135 <210> SEQ ID NO: 2
136 <211> LENGTH: 426
137 <212> TYPE: PRT
138 <213> ORGANISM: nuc. & predicted a.a. seq. of mNR4
139 <220> FEATURE:
140 <221> NAME/KEY: unsure
141 <222> LOCATION: (21)
142 <223> OTHER INFORMATION: authors are unsure about the sequence assignment
143 <221> NAME/KEY: unsure
144 <222> LOCATION: (194)
145 <223> OTHER INFORMATION: authors are unsure about the sequence assignment
146 <400> SEQUENCE: 2

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147 Met Ala Arg Pro Ala Leu Leu Gly Glu Leu Leu Val Leu Leu Leu Trp
148      1              5              10              15
W--> 149 Thr Ala Thr Val Xaa Gly Gln Val Ala Ala Ala Thr Glu Val Gln Pro
150      20              25              30
151 Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Ile Ile
152      35              40              45
153 Trp Thr Trp Ser Pro Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg
154      50              55              60
155 Tyr Phe Ser His Phe Asp Asp Gln Gln Asp Lys Lys Ile Ala Pro Glu
156      65              70              75              80
157 Thr His Arg Lys Glu Glu Leu Pro Leu Asp Glu Lys Ile Cys Leu Gln
158      85              90              95
159 Val Gly Ser Gln Cys Ser Ala Asn Glu Ser Glu Lys Pro Ser Pro Leu
160      100             105             110
161 Val Lys Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val
162      115             120             125
163 Thr Glu Leu Lys Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser
164      130             135             140
165 Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr His Tyr Thr Leu Tyr
166      145             150             155             160
167 Tyr Trp Tyr Ser Ser Leu Glu Lys Ser Arg Gln Cys Glu Asn Ile Tyr
168      165             170             175
169 Arg Glu Gly Gln His Ile Ala Cys Ser Phe Lys Leu Thr Lys Val Glu
170      180             185             190
W--> 171 Pro Xaa Ser Phe Glu His Gln Asn Val Gln Ile Met Val Lys Asp Asn
172      195             200             205
173 Ala Gly Lys Ile Arg Pro Ser Cys Lys Ile Val Ser Leu Thr Ser Tyr
174      210             215             220
175 Val Lys Pro Asp Pro Pro His Ile Lys His Leu Leu Leu Lys Asn Gly
176      225             230             235             240
177 Ala Leu Leu Val Gln Trp Lys Asn Pro Gln Asn Phe Arg Ser Arg Cys
178      245             250             255
179 Leu Thr Tyr Glu Val Glu Val Asn Asn Thr Gln Thr Asp Arg His Asn
180      260             265             270
181 Ile Leu Glu Val Glu Glu Asp Lys Cys Gln Asn Ser Glu Ser Asp Arg
182      275             280             285
183 Asn Met Glu Gly Thr Ser Cys Phe Gln Leu Pro Gly Val Leu Ala Asp
184      290             295             300
185 Ala Val Tyr Thr Val Arg Val Arg Val Lys Thr Asn Lys Leu Cys Phe
186      305             310             315             320
187 Asp Asp Asn Lys Leu Trp Ser Asp Trp Ser Glu Ala Gln Ser Ile Gly
188      325             330             335
189 Lys Glu Gln Asn Ser Thr Phe Tyr Thr Thr Met Leu Leu Thr Ile Pro
190      340             345             350
191 Val Phe Val Ala Val Ala Val Ile Ile Leu Leu Phe Tyr Leu Lys Arg
192      355             360             365
193 Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe
194      370             375             380
195 Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys

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196      385      390      395      400
197      Tyr Asp Ile Tyr Glu Lys Gln Ser Lys Glu Thr Asp Ser Val Val
198      405      410      415
199      Leu Ile Glu Asn Leu Lys Lys Ala Ala Pro
200      420      425
202 <210> SEQ ID NO: 3
203 <211> LENGTH: 1383
204 <212> TYPE: DNA
205 <213> ORGANISM: Human IL-13 receptor alpha-chain
206 <220> FEATURE:
207 <221> NAME/KEY: CDS
208 <222> LOCATION: (61)..(1338)
209 <400> SEQUENCE: 3
210      gagtctaaca cggaccaagg agtttaacac gtgcggccgg gttccgaggc gagaggctgc 60
211      atg gag tgg ccg gcg cgg ctc tgc ggg ctg tgg gcg ctg ctg ctc tgc 108
212      Met. Glu Trp Pro Ala Arg Leu Cys Gly Leu Trp Ala Leu Leu Leu Cys
213      1      5      10      15
214      gcc gcc gcc ggg gcc ggg gcc ggg gcc gcg cct acg gaa act cag cca 156
215      Ala Gly Gly Gly Gly Gly Gly Gly Gly Ala Pro Thr Glu Thr Gln Pro
216      20      25      30
217      cct gtg aca aat ttg agt gtc tct gtt gaa aac ctc tgc aca gta ata 204
218      Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Val Ile
219      35      40      45
220      tgg aca tgg aat cca ccc gag gga gcc agc tca aat tgt agt cta tgg 252
221      Trp Thr Trp Asn Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu Trp
222      50      55      60
223      tat ttt agt cat ttt gcc gac aaa caa gat aag aaa ata gct ccg gaa 300
224      Tyr Phe Ser His Phe Gly Asp Lys Gln Asp Lys Lys Ile Ala Pro Glu
225      65      70      75      80
226      act cgt cgt tca ata gaa gta ccc ctg aat gag agg att tgt ctg caa 348
227      Thr Arg Arg Ser Ile Glu Val Pro Leu Asn Glu Arg Ile Cys Leu Gln
228      85      90      95
229      gtg ggg tcc cag tgt agc acc aat gag agt gag aag cct agc att ttg 396
230      Val Gly Ser Gln Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile Leu
231      100      105      110
232      gtt gaa aaa tgc atc tca ccc cca gaa ggt gat cct gag tct gct gtg 444
233      Val Glu Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val
234      115      120      125
235      act gaa ctt caa tgc att tgg cac aac ctg agc tac atg aag tgt tct 492
236      Thr Glu Leu Gln Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser
237      130      135      140
238      tgg ctc cct gga agg aat acc agt ccc gac act aac tat act ctc tac 540
239      Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu Tyr
240      145      150      155      160
241      tat tgg cac aga agc ctg gaa aaa att cat caa tgt gaa aac atc ttt 588
242      Tyr Trp His Arg Ser Leu Glu Lys Ile His Gln Cys Glu Asn Ile Phe
243      165      170      175
244      aga gaa gcc caa tac ttt ggt tgt tcc ttt gat ctg acc aaa gtg aag 636
245      Arg Glu Gly Gln Tyr Phe Gly Cys Ser Phe Asp Leu Thr Lys Val Lys

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## VERIFICATION SUMMARY

DATE: 01/30/2002

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Input Set : N:\Crif3\RULE60\10036568.raw

Output Set: N:\CRF3\01302002\J036568.raw

L:55 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
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L:88 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:89 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:149 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:171 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:394 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:9  
L:394 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:407 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10  
L:407 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10  
L:420 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11  
L:420 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11